

IN THE CLAIMS:

The text of all pending claims, (including withdrawn claims) is set forth below. Cancelled and not entered claims are indicated with claim number and status only. The claims as listed below show added text with underlining and deleted text with ~~striketrough~~. The status of each claim is indicated with one of (original), (currently amended), (cancelled), (withdrawn), (new), (previously presented), or (not entered).

Please CANCEL claims 12-24, 27, AND 30 , without prejudice:

1. (ORIGINAL) A method for predicting gene expression sites, comprising:
calculating a distance between first and second genes on a genome sequence, wherein an expression site of the first gene is unknown, and the second gene is one of a plurality of known genes whose expression sites are known; and
determining the expression sites of the first gene based on the distance.
2. (ORIGINAL) The method according to claim 1, wherein
the calculating includes calculating the distance for each of the plurality of genes, and
the determining includes determining the expression sites of the first gene as an expression site of at least one gene that has a predetermined distance relation among the plurality of genes.
3. (ORIGINAL) The method according to claim 1, wherein
the calculating includes calculating a distance between the start position of the first gene and the start position of the second gene on the genome sequence.
4. (ORIGINAL) The method according to claim 1, wherein
the calculating includes calculating a distance between the end position of the first gene and the end position of the second gene on the genome sequence.
5. (ORIGINAL) The method according to claim 1, wherein
the calculating includes calculating a distance between the start position of the first gene and the end position of the second gene on the genome sequence.

6. (ORIGINAL) The method according to claim 1, wherein the calculating includes calculating a distance between the end position of the first gene and the start position of the second gene on the genome sequence.

7. (ORIGINAL) The method according to claim 1, wherein the calculating includes calculating a distance between first and second positions, the first position being between the start and end positions of the first gene on the genome sequence, and the second position being between the start and end positions of the second gene on the genome sequence.

8. (ORIGINAL) The method according to claim 1, wherein the calculating includes calculating a distance between a position between the start and end positions of the first gene and the start position of the second gene on the genome sequence.

9. (ORIGINAL) The method according to claim 1, wherein the calculating includes calculating a distance between a position between the start and end positions of the first gene and the end position of the second gene on the genome sequence.

10. (ORIGINAL) The method according to claim 1, wherein the calculating includes calculating a distance between the start position of the first gene and a position between the start and end positions of the second gene on the genome sequence.

11. (ORIGINAL) The method according to claim 1, wherein the calculating includes calculating a distance between the end position of the first gene and a position between the start and end positions of the second gene on the genome sequence.

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25. (ORIGINAL) A computer program product including computer executable instructions, for predicting gene expression sites, wherein the instructions, when executed by the computer, cause the computer to perform:

calculating a distance between first and second genes on a genome sequence, wherein an expression site of the first gene is unknown, and the second gene is one of a plurality of genes whose expression sites are known; and

determining the expression sites of the first gene based on the distance.

26. (ORIGINAL) The computer program product according to claim 25, wherein the determining include determining the expression sites of the first gene as an expression site of at least one gene that has a predetermined distance relation among the plurality of genes.

27. (CANCELLED)

28. (ORIGINAL) An apparatus for predicting gene expression, comprising:
a calculation unit that calculates a distance between first and second genes on a genome sequence, wherein an expression site of the first gene is unknown, and the second gene is one of a plurality of genes whose expression sites are known; and
a determination unit that determines the expression sites of the first gene based on the distance.
29. (ORIGINAL) The apparatus according to claim 28, wherein
the calculation unit calculates the distance for each of the plurality of genes, and
the determination unit determines the expression sites of the first gene as an expression site of at least one gene that has a predetermined distance relation among the plurality of genes.
30. (CANCELLED)